99/787323 532 **O**d PCT/PTO 16 MAR 2001

## ABSTRACT OF THE DISCLOSURE

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## **Multiple Sequencing Method**

The present invention provides a method for identifying a nucleic acid utilizing a run-off sequencing reaction of a relatively short portion of the nucleic acid. The method can be utilized, for example, to identify an EST from only a small portion of the EST and in an analysis of nucleotide polymorphisms.